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Genome Biology

OPINION

Q & A: the Snyderome

Michael Snyder*

Abstract

Michael Snyder answers *Genome Biology*'s questions on the human and professional stories underlying his Snyderome integrative omics project.

Much excitement has surrounded the potential to apply high-throughput technologies to personalized medicine. The promise of omics in the clinic could mean not only tailored treatments but early pinpointing of disease states. In the current issue of *Cell*, Michael Snyder (Box 1) and colleagues present what they term an 'iPOP' (integrative Personal Omics Profile), which includes the genome, transcriptome, proteome, metabolome and auto-antibody profile of a single individual assayed over a 14-month period [1].

And who was the individual that featured as the subject of this iPOP? Michael Snyder himself, who argues that a single individual when studied over a length of time can make for a powerful study. Indeed, by chronicling health states over the time course, extensive disease-associated molecular changes were reported, including differential allele-specific expression and unexpected RNA-editing events.

In a Q & A with *Genome Biology*, Prof. Snyder explains the background to the 'Snyderome' project and gives an insight into the impact of self-omics on his way of life.

What inspired you to undertake the 'Snyderome' project, and did you choose yourself as the subject mainly as a matter of convenience or because of a desire to know your own biology in great detail?

MS: It really started as a matter of convenience and a proof of principle experiment. When I moved to Stanford, I planned to perform whole omics profiling on a number of diseases. Just to get started, I chose myself as a test subject because of the availability of material, and because it would be easy to enroll in a study and get informed consent.

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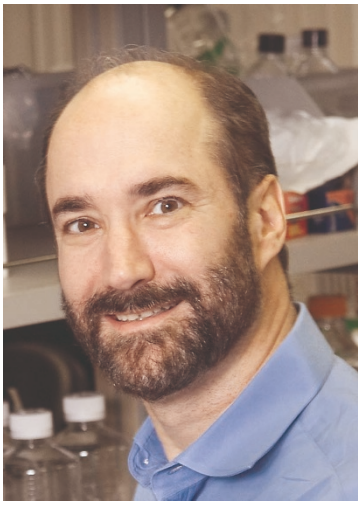

Box 1. About Michael Snyder (MS)

Michael Snyder is the Stanford Ascherman Professor and Chair of Genetics and the Director of the Center of Genomics and Personalized Medicine. He is a leader in the field of functional genomics and proteomics, and the milestones achieved by his laboratory include the first genome (*Acinetobacter*) to be sequenced using high-throughput DNA sequencing technologies, the first large-scale analysis of gene function, and the invention of RNA-Seq, ChIP-chip and paired-end sequencing. He is the recipient of the Connecticut Medal of Science and the Pioneer Award in Proteomics.

It so happens that I had a cold (*Rhinovirus* infection) when I first gave blood, and this led to the idea of performing a simple longitudinal profile in which we could compare infected and healthy states. Of course, it is now 2 years later and, over these 2 years, as many new questions have arisen as answers.

How did you obtain funding for this project?

MS: The project was mostly paid for by the funding I received to set up my new lab at Stanford. We also have a NIH center of excellence grant for analyzing genomes and some of the tools we developed for that were applied to this project.

Were there any datasets in particular that you had reservations about obtaining?

MS: No, not really.

Was there any other component of your biology that you ideally would have included in the project but were not able to because of technical, financial or time limitations?

MS: There are a number of datasets that would be great to add. First, we would like (and still plan to) carry out a detailed DNA methylome analysis. When we started this was very expensive so we thought we would wait a bit while the price drops, which has now happened and so we are ready to do it.

It would also be nice to perform detailed profiling on each cell type in the blood, but that would require a lot more effort. Similarly, it would have been great to analyze urine and breath as well as blood. I would additionally like to perform an exposome analysis to see what chemicals I have been exposed to, and to obtain several microbiome studies.

I would like to have obtained a better analysis of the viruses, as the complexity of microbes that were present would have been nice to know. We tried taking nasal swabs but were not successful in cultivating the suite of pathogens I had when I was infected. We only know in general types of viruses (*Rhinovirus*, respiratory syncytial virus), but I suspect that additional pathogens might have been present.

Finally, there are several ChIP-Seq experiments that would have been great to perform. So in fact the list goes on and on and there is much more to do.

What did your peers think of the project? Are others considering a similar analysis on themselves?

MS: The vast majority of my peers are extremely supportive and think the project is terrific. Indeed, most concur with me that we need to generate many more profiles of a similar type and that this approach is the future of medicine. In fact, many of my peers volunteered to help on the project without me asking.

Some people think that you cannot learn anything by analyzing a single person. However, they do not realize that longitudinal profiling is ideal for personalized medicine because the goal is to identify physiological states that deviate from your healthy state, as occurs during a viral infection or the onset of diabetes.

How did you convince your mother to agree to take part in the project, and to what extent do you feel an extra burden of responsibility by including her?

MS: My mother is a curious person by nature and extremely positive about science so it did not take much convincing. In fact, just the opposite - she was eager to participate. I did not feel too worried about including her as she is 83 (and going strong), so I imagine that her genome might be able to tell us a lot of good things, especially with respect to what variants are not likely to be harmful. As an example, I have a variant in my telomerase gene that is the same one as appears in aplastic anemia patients. My mom has the exact same mutation, so I am not too worried about it.

We understand that you have young children - do you think self-omicing will be commonplace by the time they reach adulthood?

MS: At some level omics profiling will be more commonplace. The concept that when you get a medical exam you are given a blood test that measures only a handful of components strikes me as very primitive, and was one of the motivations for performing this study. Why measure five or ten items when you can measure 40,000 and potentially learn a lot more?

And would you encourage your children to have their omes sequenced?

MS: I think it is up to them to decide if they want to get their genomes sequenced. On one hand, there are many useful things that can be learned. However, I would advise against it if they turn out to be worriers because we all have many deleterious mutations.

How publicly available are the data going to be and how comfortable are you with this level of availability?

MS: All of the data have already been submitted to public databases. I am quite comfortable with this. In fact, people see my talk and frequently offer me useful insights about my variants.

In what unexpected ways has the project affected your life?

MS: My genome sequence predicted I was at risk for diabetes, which was unexpected. During the course of the study my glucose level shot up (interestingly right after a respiratory syncytial virus infection) and I was classified as diabetic. The elevated glucose level did not come down right away but, after changing my diet quite dramatically, increasing my exercise and taking low doses of aspirin, it did gradually come down to a level fairly close to where I started. I still maintain these lifestyle changes, and my eating habits are now completely different to before the discovery of my diabetes.

I looked into obtaining supplemental life insurance, but discovered that the premiums for an individual with diabetes, even though it is now well-managed, are cost-prohibitive.

If you had to make the decision again, would you still embark on this project? With hindsight, what changes would you make to the study?

MS: Yes, and I would have documented my eating habits and daily activities better.

If you could sequence the genome of one person - living or dead - who would it be?

MS: My dad (who is deceased).

Competing interests

Michael Snyder is a founder and consultant for Personalis, a member of the scientific advisory board of GenapSys and a consultant for Illumina.

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